Amendments to the Claims

1-45. (Cancelled)

46. (Original) A method of determining loss of function of a nucleic acid encoding a regulatory molecule in a test cell comprising:

selecting a first nucleic acid molecule encoding a regulatory molecule;

selecting a set of second nucleic acid molecules whose expression is induced or repressed by the regulatory molecule in normal cells;

hybridizing a transcription indicator of a test cell to a set of nucleic acid probes, wherein the transcription indicator is selected from the group consisting of mRNA, cDNA and cRNA, wherein each member of the set of nucleic acid probes comprises a portion of a nucleic acid molecule which is a member of the set of second nucleic acid molecules;

detecting the amount of transcription indicator which hybridizes to each of said set of nucleic acid probes;

identifying a test cell as having lost function of the regulatory molecule if (1) hybridization of the transcription indicator of the test cell to a probe which comprises a portion of a nucleic acid which is induced by the regulatory molecule is lower than hybridization using a transcription indicator from a normal cell, or (2) hybridization of the transcription indicator of the test cell to a probe which comprises a portion of a nucleic acid which is repressed by the regulatory molecule is higher than hybridization using a transcription indicator from a normal cell.

47. (Original) The method of claim 46 wherein the regulatory molecule is p53.

48. (Original) The method of claim 46 wherein the test cell is a breast cell.

49. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 4 genes which are activated or repressed by p53.

50. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 10 genes which are activated or repressed by p53.

51. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 20 genes which are activated or repressed by p53.

52. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 30 genes which are activated or repressed by p53.

53. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 100 genes which are activated or repressed by p53.

54. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 250 genes which are activated or repressed by p53.

55. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 300 genes which are activated or repressed by p53.

56. (Original) The method of claim 46 wherein the set of nucleic acid probes

comprises nucleic acid sequences which comprise a portion of at least 400 genes which are activated or repressed by p53.

57. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 500 genes which are activated or repressed by p53.

58. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 750 genes which are activated or repressed by p53.

59. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 1000 genes which are activated or repressed by p53.

60. (Original) The method of claim 46 wherein the nucleic acids which each comprise a portion of a gene which is activated or repressed by p53 are selected from those shown in Table 3.

61. (Original) The method of claim 46 wherein the nucleic acid probes are attached to a solid support.

62. (Original) The method of claim 46 wherein the nucleic acid probes are arranged in an array.

63. (Original) The method of claim 62 wherein the array comprises nucleic acid probes which are portions of at least 250 genes which are either p53-induced or p53 -repressed.

64. (Original) The method of claim 62 wherein the array comprises nucleic acid probes which are portions of at least 6000 different genes.

65. (Currently amended) The method of claim 46 wherein for each of the following genes at least one of the nucleic acid probes in the set comprises a portion ~~of each of~~ thereof: Cyclin G, GADD45, IGF-BP3, p21 $^{WAFI/CIP1}$, Thrombospondin, C-myc, and PCNA, as defined in Table 2.

66. (Currently amended) The method of claim 46 wherein for each of the following genes at least one of the nucleic acid probes in the set comprises a portion ~~of each of~~ thereof: Bax, Cyclin G, GADD45, IGF-BP3, p21 $^{WAFI/CIP1}$, Thrombospondin, C-myc, and PCNA, as defined in Table 2.

67. (Original) The method of claim 46 further comprising the step of:

determining the sequence of p53 genes in the test cell to confirm the p53 status of the cell.

68. (Original) The method of claim 46 wherein a test cell is identified as p53-negative if hybridization is at least 3-fold different between compared samples.

69. (Original) The method of claim 46 wherein a test cell is identified as p53-negative if hybridization is at least 5-fold different between compared samples.

70. (Original) The method of claim 46 wherein a test cell is identified as p53-negative if hybridization is at least 10-fold different between compared samples.

71. (Original) A method of diagnosing neoplasia of a test cell comprising:

hybridizing a transcription indicator of a test cell to a set of nucleic acid probes, wherein the transcription indicator is selected from the group consisting of mRNA, cDNA and cRNA, wherein the set of nucleic acid probes comprises at least one nucleic acid molecule which is a portion of a gene which is activated by or repressed by p53;

detecting the amount of transcription indicator which hybridizes to each of said set of

nucleic acid probes;

identifying a test cell as neoplastic if (1) hybridization of the transcription indicator of the test cell to a probe which is a p53-activated gene is lower than hybridization using a transcription indicator from a normal cell, or (2) hybridization of the transcription indicator of the test cell to a probe which a p53-repressed gene is higher than hybridization using a transcription indicator from a normal cell.

72. (Original) The method of claim 71 wherein the test cell is a breast cell.

73. (Original) The method of claim 71 wherein at least 4 of said probes comprise portions of genes which are p53-activated or p53-repressed.

74. (Original) The method of claim 71 wherein at least 10 of said probes comprise portions of genes which are p53-activated or p53-repressed.

75. (Original) The method of claim 71 wherein at least 20 of said probes comprise portions of genes which are p53-activated or p53-repressed.

76. (Original) The method of claim 71 wherein at least 30 of said probes comprise portions of genes which are p53-activated or p53-repressed.

77. (Original) The method of claim 71 wherein at least 50 of said probes comprise portions of genes which are p53-activated or p53-repressed.

78. (Original) The method of claim 71 wherein at least 75 of said probes comprise portions of genes which are p53-activated or p53-repressed.

79. (Original) The method of claim 71 wherein at least 100 of said probes comprise portions of genes which are p53-activated or p53-repressed.

80. (Original) The method of claim 71 wherein at least 250 of said probes comprise portions of genes which are p53-activated or p53-repressed.

81. (Original) The method of claim 71 wherein at least 300 of said probes comprise portions of genes which are p53-activated or p53-repressed.

82. (Original) The method of claim 71 wherein at least 500 of said probes comprise portions of genes which are p53-activated or p53-repressed.

83. (Original) The method of claim 71 wherein at least 750 of said probes comprise portions of genes which are p53-activated or p53-repressed.

84. (Original) The method of claim 71 wherein at least 1000 of said probes comprise portions of genes which are p53-activated or p53-repressed.

85. (Original) The method of claim 71 wherein the nucleic acid probes are attached to a solid support.

86. (Original) The method of claim 71 wherein the nucleic acid probes are arranged in an array.

87. (Original) The method of claim 86 wherein the array comprises nucleic acid probes which are portions of at least 250 different genes.

88. (Original) The method of claim 71 wherein the array comprises nucleic acid probes which are portions of at least 6000 different genes.

89. (Currently amended) The method of claim 71 wherein for each of the following genes at least one of the nucleic acid probes in the set comprises a portion ~~of each of~~ thereof: Bax, Cyclin G, GADD45, IGF-BP3, $p21^{WAF1/CIP1}$, Thrombospondin, C-myc, and PCNA, as defined in Table 2.

90. (Currently amended) The method of claim 71 wherein for each of the following genes at least one of the nucleic acid probes in the set comprises a portion ~~of each of~~ thereof: Bax, Cyclin G, GADD45, IGF-BP3, $p21^{WAF1/CIP1}$, Thrombospondin, C-myc, and PCNA, as defined in Table 2.

91. (Original) The method of claim 71 further comprising the step of:

determining the sequence of p53 genes in the test cell to determine the p53 genotypic status of the cell.

92. (Original) The method of claim 71 wherein a test cell is identified as neoplastic if hybridization is at least 3-fold different between compared samples.

93. (Original) The method of claim 71 wherein a test cell is identified as neoplastic if hybridization is at least 5-fold different between compared samples.

94. (Original) The method of claim 71 wherein a test cell is identified as neoplastic if hybridization is at least I 0-fold different between compared samples.

95-129. (Cancelled)